

1535 TGTCTTCACAGCCGCTTCGCTCGCTCGGCATCCACAGTCCACCCGCTG 1584
501 VAtaAgpGLeuAspAserPheGlnGluLeuProAspLeuProGlyLe 517
1585 GAGAGCGTGGCCAGCCCTCCGAGGCTTCGAGAGGCTTCGAGTCCGAGC 1634
517 vtrpLeuGLeuAlaPhePheSerProPfrThrLeuLeuArgGlyGly 534
1635 GAGGCTGACAGGCTTCCTGAGCGTGGAGATGATGATGATGATGATG 1684
534 LeuAspProLeuLeuLeuArgGlyLeuLeuAlaArgProAlaLeuLeu 550
1685 GTTGGAGCCCTATATACAGGCTCTCTGACAGCCAGCCAGCCAGG 1734
551 ValGlnGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 567
1735 GTCCAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1784
567 yserAserSerThrLeuAspLeuAlaSerIleLeuLeuLeuLeuGly 584
1785 GTCCAT 1834
584 rGAspGluLeuProGlyProGlyTrpGlnGlnGlnGlnGlnGlnGln 600
1835 GACAGCGGCTGGAGCTGAGCTGATGATGATGATGATGATGATGATG 1884
601 ProAspGlnThrProAlaAspAspSerThrAlaLeuAspArgGly 617
1885 CCGCTGCTGGACACCCGCTGACCTGACCTGACCTGACCTGACCTG 1934
617 vGluAlaAspGlnThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 634
1935 GGTGGCCGACAGATCTCGATCTGTACAGGATCTGTACAGGATCTG 1984
634 vTrpLeuGlnGlyLeuAlaGluAspPheLeuProAspAlaPheGly 650
1985 TCTGGCTGGAGGCTTAGCTGAAGATCTCTCCGAGGAGCTCGACAGG 2034
651 ProGluPheAlaCysLeuLeuLeuGlyGlnGlnGlnGlnGlnGlnGln 667
2035 CCCTGTGTCTGCTGCTCANTGTGGAGAGAGAGAGAGAGAGAGAG 2084
667 yserPhePhePhePhePhePhePhePhePhePhePhePhePhePhe 684
2085 TGACCTGGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2134
684 rGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 700
2135 GTGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2184
2185 CTACAG 2234
717 pPheLeuSerCysAspSerIleThrGlyMetLeuLeuGlnGlnGln 734
2235 CTCTGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2284
734 ThrThrPheThrAspAspGlyGlyGlyGlyGlyGlyGlyGlyGly 750
2285 AAGCTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2334
751 GAspPheValHisCysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 767
2335 GGGAGCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2384
767 rCysValHisGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 784
2385 CTGCGGAG 2434
784 LeuGlnGlyGlyPhePhePhePhePhePhePhePhePhePhePhe 800
2435 AG 2484

seq_name: gb_pat: A8092419

seq_documentation_block: 3048 bp DNA PAT 08-SEP-2000
LOCUS A8092419
DEFINITION Sequence 2 from patent US 5998153.
ACCESSION A8092419
KEYWORDS A8092419.1 OT:10019173
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3048)
AUTHORS Baker, J.R., Jr. and Koenig, R.J.
TITLE Thymidylate synthase gene and its use in the treatment of cancer.
PATENT: US 5,998,153.
FEATURES
Location/Qualifiers
source 1..3048
/organism="unknown"
BASE COUNT 671 a 930 c 881 g 566 t
ORIGIN

alignment_scores: Quality: 4528.00 Length: 848
Ratio: 5.365 Gaps: 0
Percent Similarity: 99.528 Percent Identity: 99.175
alignment_block:
US-08-482-402A-3_COPY_1_848 x A8092419
Align seg 1/1 to: A8092419 from: 1 to: 3048

1 MetAagLeuAlaLeuSerValThrThrLeuValMetAlaCysThrGln 17
73 ATGAGAGCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
17 ValAlaPheProPheThrIleSerArgGlyGlyGlnLeuLeuLeuLeu 34
123 AGCTCTCTCCCTCTCATCTCGAGAGAGAGAGAGAGAGAGAGAGAG 172
34 rGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 50
173 CTGAGAGAGCTCTGCTGCTCTAGGCTCTGAGGAGAGAGAGAGAGAG 222
51 MetPheThrMetGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 67
223 GACACCGCATGTTAGCCAGGATGAGAGAGAGAGAGAGAGAGAGAGAG 272
67 rGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 84
273 CTTTTCTCCAGTCACTCTCTCTTTTTCGAGAGAGAGAGAGAGAGAG 322
84 rGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
323 CGGAGAGTGTATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 372
372 MetThrGlyGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 400
373 ATGAAAG 422

623 GOTTGAGTACGCGGAGCTGGAGCCCGGCTCTGTACAGCGGTC 672
201 ProleupPheArgLeuValThrArgHisValIleGlnValSerAs 217
673 CAGTACGCGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722
217 AGLeuValThrAspAspArgArgArgArgArgArgArgArgArg 234
723 TGGTGTGTGCAGATGATGATGATGATGATGATGATGATGATG 772
234 TGGTGTGTGTGCAGATGATGATGATGATGATGATGATGATG 792
773 GAGATATGATGATGATGATGATGATGATGATGATGATGATG 822
251 AAlaAlaPheGlyGlySerAspGlyMetThrGlyIleGlnIle 267
823 CGCTCTCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 872
267 GAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 284
873 CCGATGATGATGATGATGATGATGATGATGATGATGATGATG 922
284 LeuAlaGlySerPheGlyThrGlySerGlyGlyGlyGlyGly 300
923 CGCGCTGTCTGCGCTGTCTGCGCTGTCTGCGCTGTCTGCGCT 972
301 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
973 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
317 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 334
1023 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1072
334 TAlaLeuLeuLeuGlyLeuLeuGlyLeuLeuGlyLeuLeu 350
1073 GCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1122
351 ArgValHisGlyValLeuLeuLeuGlyValArgLeuLeuPhe 367
1123 GCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1172
367 LProPArgAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAla 1200
1173 GCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1222
384 LuthArgGlyProCysPheLeuAlaGlyValGlyValArgLeu 400
1223 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1272
401 ProSerLeuThrAlaLeuAlaLeuAlaLeuAlaLeuAlaLeu 417
1273 CCGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1322
417 AlaAlaAlaLeuAlaLeuAlaLeuAlaLeuAlaLeuAlaLeu 434
1323 GCGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1372
434 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 450
1373 ACGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1422
451 ArgAspGlyIleProArgIleLeuGlyProGlyAlaPheGlyGly 467
1423 AGGATATGATGATGATGATGATGATGATGATGATGATGATG 1472
467 LysArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 484
1473 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 500
484 AlPheSerThrAlaAlaPheArgPheGlyHisAlaThrIleHis 500
1523 TGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1572

434 yrlgdluabakdylvavlaiglvaaeulielgdllelthprrleu 450
 1341 acagagprrytlleppakglttggggccgtccgacagatcatcacctts 1390
 451 acagagprrytlleppakglttggggccgtccgacagatcatcacctts 1390
 1391 agggatattacatccacagatcttggagccggccgtccacagatcagct 1440
 467 gclgpyrtygluclvtyrfaupserthralaaenprrthvalseraunv 484
 1441 gggtccatattgagatgacatccgacacccatccgttccacag 1490
 484 alpksserthrtaalaahpakghphelgylhlaalrthrllehprrleu 500
 1491 ttttttccacacccgtcttccgtctccgcatccgacatccacccgtts 1540
 501 valaagagluenaplaaserpheclndluilaprraopmlenprrdyle 517
 1541 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1590
 517 yrlgdluabakdylvavlaiglvaaeulielgdllelthprrleu 534
 1591 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1640
 534 ylaenaprrleu1leahgdyllenuleu1laarprolatayleucln 550
 1641 yrlgdluabakdylvavlaiglvaaeulielgdllelthprrleu 1690
 551 valagldglnleu1leahgdyllenuleu1laarprolatayleucln 1740
 1691 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1790
 567 userasaserthrleuaplaaser1leahgdyllenuleu1laarprolatayleucln 1790
 1741 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1840
 584 rfaupserthrtaalaahpakghphelgylhlaalrthrllehprrleu 600
 1791 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1840
 601 prokgldglnleu1leahgdyllenuleu1laarprolatayleucln 617
 1841 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1890
 617 rfaupserthrtaalaahpakghphelgylhlaalrthrllehprrleu 634
 1891 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1940
 634 altprrdylleu1leahgdyllenuleu1laarprolatayleucln 650
 1941 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 1990
 651 prokgldglnleu1leahgdyllenuleu1laarprolatayleucln 667
 1991 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 2040
 667 rfaupserthrtaalaahpakghphelgylhlaalrthrllehprrleu 684
 2041 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 2090
 684 rfaupserthrtaalaahpakghphelgylhlaalrthrllehprrleu 700
 2091 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 2140
 701 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 717
 2141 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 2190
 717 rfaupserthrtaalaahpakghphelgylhlaalrthrllehprrleu 734
 2191 gthgagaggggtggagccagcttcttggacagacaccccgacgttcccggt 2240
 734 luthr-phepprrleu1leahgdyllenuleu1laarprolatayleucln 750

seq_name: gb_pat:023825

seq_documentation_block: 2546 bp

Accession: E23825

Definition: Antigen for immunoscreening antihuman thyroid peroxidase antibody

Keywords: E23825, GI:13024570

Source: JP 1999/04833-A/1

Organism: unidentified

Reference: Masao F.

Antigen for immunoscreening antihuman thyroid peroxidase antibody

Title: Patent: JP 1999/04833-A 1 09-APR-1999

Journal: SBIL INC identified

Comment: PN 09-APR-1999

PD 09-APR-1999

PF 19-SEP-1997 JP 1997273743

PI MASAO FUKUSHIMA

PC G01N33/53, C12N9/08, C12N15/09, G01N33/564, C12N9/08

PC C12N15/51, C12N9/08

CC Strandedness: Double;

CC Topology: Linear;

FI Key

FT source

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

alignment_scores:

Quality: 4495.00

Ratio: 5.336

Percent Similarity: 99.292

Percent Identity: 98.349

alignment_block:

134 auPProPheLeuProProLyCyProPheThrCysLeuAlaLeu 150
473 TCCTCTACATGCTGCCCAAAATGCCCAACATCTGCTGGCAACA 522
151 TTTATATPCTTCTGCTGATGATGATGATGATGATGATGATGAT 167
523 TACAGCCCATCATAGAGGCTTGCACACAGACAGACACCCCATGG 572
167 yAlaSerAsnThrAlaLeuAlaLeuTTPLeuProProValTyrGlu 184
573 GCTCTCAACACGGCTCTGGCATGCTGCTGCTGCTGCTGCTGCT 622
184 TlyGlyTyrTlePhePhePhePhePhePhePhePhePhePhe 600
623 CTTTCAATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 672
201 ProLeuProProValAlaGluValThrAlaGluValTleGluVal 217
673 CAGCTGCCCTCCGGTCCGGAGCTGAGCATGATGATCATCATGAT 722
217 GCUValThrAspAsnAspAspAspAspAspAspAspAspAsp 234
723 TAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 772
234 TlyGlyTyrTlePhePhePhePhePhePhePhePhePhePhe 250
773 GACATATGCTGACATGACATGACATGACATGACATGACATGAC 822
823 CTTGCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 872
267 ProCysPheProTleGluLeuProGluGluAlaLeuProAlaGly 284
873 CCCTATTTTCCATACATCTCCGAGAGGGGGGGGGGGGGGGGG 922
284 AlaCysLeuProPhePheTyrArgSerSerAlaCysGlyThrGly 300
923 CGCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 972
301 GylGlyAlaLeuPheGlyAsnLeuSerThrAlaAsnProArgGln 317
973 GAGAGGCTCTTGGAGAGCTGTCCAGAGCCAGCCAGCCAGCCAG 1022
317 GAsnGlyLeuThrSerPheLeuSerThrValTyrGlySerP 334
1023 GAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1072
334 roAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 350
1073 CGCTCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122
351 ArgGlnHisGlyArgLeuArgAspSerGlyArgAlaLeuProPhe 367
1123 GGGTCTCAGCGGGCTCTGGAGAGCTCGAGCGGGCTCTGGCT 1172
367 TProPheArgAlaProAlaCysAlaProProGluPheProGly 384
1173 GCGGACAGCGGGCTCTGCTCTCTGCGCGAGAGCGGGCTCTG 1222
384 LuThrArgGlyProCysPheLeuAlaGlyAspGlyArgAlaSer 400
1223 AAGCCAGCGGGCTCTGCTCTCTGCGCGAGAGCGGGCTCTG 1272
401 ProSerLeuThrAlaLeuHisThrLeuLeuGluLeuLeuArgLe 417
1273 CCGCTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1322
417 GAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 434
1323 GGGCGCGGGCTCTAGAGGGCTCTAGAGGGCTCTAGAGGGCTCT 1372
1372 yGlyGluAlaLeuArgGlyValGlyAlaLeuLeuGlnTleThrLeu 450

1373 ACTAGAGAGCGCGCGAGAGCTCTGGGGCTCTGCAACAGATCAT 1422
451 ArgAspGlyThrLeuProGluLeuLeuLeuLeuLeuLeuLeuLeu 467
1423 AGGATATCATCTCCAGAGATCTCTGGAGAGAGAGCTCTCAGAG 1472
467 TlyProGluGluGlyTyrArgSerPheAlaLeuProPheValSer 484
1473 GGGTCTCTATGAAGGCTATGATCTCCAGCCAGCCAGCTGTGCA 1522
484 AlPheSerThrAlaAlaPheAspPheGlyAlaAlaThrTleLeu 500
1523 TGTCTCCACAGCGGCTTCCGGCTTGGCGATGCGATGATCCGCT 1572
501 ValArgGluGluGluGluGluGluGluGluGluGluGluGluGlu 517
1573 GTGAGAGAGCTGGAGCGGAGCTTCCAGAGAGAGAGAGAGAGAG 1622
517 ThrLeuLeuGluTleAlaPhePheSerProPhePheLeuAlaGly 534
1623 GTGGCTGCAAGAGCTTTCTCAGCGATGACATTTACTCGTGA 1668
534 TlyLeuAspProLeuTleArgGlyLeuLeuAlaArgProAlaGly 550
1668 1668
551 ValGlnAspGlnLeuLeuAsnGlnGluLeuThrGluArgGluPhe 567
1668 1668
567 uSerAsnSerSerThrLeuAspLeuAlaSerTleAsnLeuGln 584
1668 1668
584 ArgAspGlyLeuProGlyTyrPheGluThrArgGluPheCysGly 600
1669 GGTACAGATGAGAGAGAGAGCTTGGCGCTG 1701
601 ProArgLeuGluThrProAlaAspLeuSerThrAlaAlaSerArg 617
1701 CTTGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1751
617 yValAlaAspPheTleLeuAlaLeuPheTyrGlySerPhePro 634
1752 CTTGCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1801
634 AlTlePheGluGlyLeuAlaGluLeuAlaProArgAlaArgThr 650
1801 TCTGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1851
651 ProLeuPheAlaCysLeuLeuGlyGlyGlyGlyGlyGlyGlyGly 667
1852 CCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1901
667 yAspPhePhePhePhePhePhePhePhePhePhePhePhePhe 1901
1902 TACCTGTTTGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1951
684 ArgGluLeuLeuAlaGlySerLeuSerArgValTleCysAspAsn 700
1952 GTAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2001
701 LeuThrArgValProMetAspAlaPheGlnValGlyGlyPhePro 717
2002 CTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2051
717 pPheGlyuSerCysAspSerTleThrGluLeuLeuAlaLeuArg 734
2052 CTTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2101
734 LuThrPheProTleAspPhePhePhePhePhePhePhePhePhe 2150

284 brAlaCysLeuProPheThrArgSerSerAlaAlaCysGlyThrGluValp 300
900 CTCAGCGCTCGCTCTTACCGCTCTCCCGCTCTGCGCTGCGCTGCGCTG 317
301 GluGlyValLeuPheGlyLeuSerThrAlaAlaProArgGlyGlnG 317
950 CAGAGCTGCTCTTGGCGACCTCTCTCCAGCAATCGAGCAGCAGAT 999
317 TAmcYLeuThrSerPheLeuAlaAlaSerThrValTyrGlySerSeP 334
1000 GAACTGCTGAGCTCTCTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTG 1049
334 ToAlaLeuGluAlaGlyLeuAlaGlySerThrAlaGlyLeuLeu 350
1050 CTCGGCTTGGAGAGCCTGCGCACCTGGACGCTGGCGAGCCTGCTG 1099
351 ATyAlaHlaGlyValGluAlaGlySerThrValTyrGlyLeuProPhe 367
1100 GTCGTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1147
367 LProProAlaAlaAlaCysAlaProLeuProGlyLeuProGly 384
1148 GCGACGCCCTGCGCTCTGAGAGCTGCTGAGCGCA 1187
384 LArgGlyCysPheLeuAlaGlyAspGlyValGlyAlaSerGluVal 400
1188 CGACGCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1237
401 ProSerLeuAlaLeuThrLeuLeuLeuLeuLeuLeuLeuLeuLeu 1277
1238 CTCGCTGCGAGCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1287
417 ATyAlaAlaLeuAlaLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 434
1288 GGGCTTGGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCT 1337
434 YGlnGlnAlaGlyValGlyAlaLeuAlaLeuAlaLeuAlaLeuAla 450
1338 AGCGAGCGCGCTGAGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCT 1387
451 ArgAlaPyrThrProGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 467
1388 AGGCTTGGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCT 1437
467 LcYrThrGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 484
1438 GGGCTTGGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCT 1487
484 ATPheSerThrAlaAlaPheGlyPheGlyLeuLeuLeuLeuLeuLeu 500
1488 TCTTCT 1537
501 ValArgPheThrAlaAlaPheGlyPheGlyLeuLeuLeuLeuLeuLeu 517
1538 GTTACGCGCT 1587
517 TTPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 1637
1588 GGGCTTGGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCTCTGAGCGCT 1687
534 LyrAlaPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 550
1638 GTTACGCGCT 1687
551 ValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 567
1688 GTTACGCGCT 1737
567 UserAlaSerSerThrLeuAlaAlaAlaAlaAlaAlaAlaAlaAla 584
1738 GTTACGCGCT 1787
584 TArgAlaGlyLeuProGlyTyrAlaAlaAlaAlaAlaAlaAlaAlaAla 600

1788 GGATCATGCTCTACGACATCATGATGAGAGAGTCTGTGGCTG 1837
601 ProArgLeuThrProAlaAspLeuSerThrAlaAlaSerArgSe 617
1838 TCACCTCTGGAGACACACCTGAGCTGACACAGGCGATCTGCACAGAG 1887
617 PAlaAlaAlaCysLeuAlaAspLeuTyrGlySerProAlaPheLeu 634
1888 CATGCTCACACAGATATGACATATACAGCATCTGCACACATGAC 1937
634 ATTPheGlyLeuAlaGlnAlaPheLeuProArgAlaAlaGlyThr 650
1938 TCTGCTGGAGAGCTTGGCTGAAAGTCTTGGCGGGGCGCTGCTGCT 1987
651 ProSerPheAlaCysLeuAlaGlyGlyGlyGlyGlyGlyGlyGlyGly 667
1988 CTTCTGTTTCATGATCATCTGGAGCAGCAGAGCTCTGAGGATGG 2037
667 TArgPhePhePhePheGlnSerLeuAlaPhePhePhePhePhePhe 684
2038 GCGAGCTTTTGGTGAGACACCACTCTCTACAGCTCTAGAGGC 2087
684 TGGTLeuGlyLeuAlaSerLeuSerAlaGlyValCysAspAlaPhe 700
2088 AGAATCAAAAGCACTTACTACCTGGGCTCATCTGTGCACACCTGGA 2137
701 LeuThrGlyValProMetAlaAlaPheGlnGlyGlyPheProGln 717
2138 CTACACAGAGTCTGTGCTCTGATATGGAAGTTCGCCCAAGA 2187
717 PheGlyLeuCysArgSerLeuThrGlyMetLeuLeuGluAlaThr 734
2188 CTTTGATCTCTGAGCATCTCCAGCATCTGAACTATGGAGG 2237
734 LThrPheProGlnAlaAspLeuPheCysGlyPheProLeuSerValGln 750
2238 AGACTTCTCCACAGATACAGATGCTCTCTCCAGAGAGGTGGACAT 2287
751 GlyAspPheValHisCysGlyGlyLeuSerGlyValGlyValTyrSe 767
2288 GGAATTTGTGCTGAGAGAGTCTGGAGAGTCTGTGTATCT 2337
767 CysArgGlyGlyTyrGlyLeuGlyGlyGlyGlyGlyGlyGlyGly 784
2338 CTTTCTCTGATCATCTGAGCATCTCCAGCATCTGAACTATGGAGG 2387
784 InGlyLeuPhePhePhePhePhePhePhePhePhePhePhePhe 800
2388 AGAGAGGTGGAGCTCGACATCTCTCTGTATGAGATGTATGTAGGT 2437
801 AlaAspGlyValHisProPheCysHisAlaSerAlaCysArgAnth 817
2437 GAGATCTGACACCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2487
817 TArgGlyGlyPheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 834
2488 CAGAGAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2537
834 spGlyValGlyThrCysAlaAspSerGlyGlyLeuProArgValThr 848
2538 ATGAGAGCTCTGATCATCTGAGCATCTGAACTATGGAGGATCC 2581

seq_name: gb:ro:RATTPOR
seq_documentation_block:
LOCUS RATTPOR 2777 bp mRNA ROD
DEFINITION Rat thyroid peroxidase (TPOR) mRNA, 3' end.
ACCESSION M31655
VERSION 1 GI:207434
KEYWORDS Rat thyroid peroxidase.
SOURCE Rat thyroid cell line FRTL-5. cDNA to mRNA.
ORGANISM Rattus norvegicus


```

371  TATATTCGACACAGCGTCAATTCAGTATGAGAAATCTTCAGAAAT 420
109  hrdgluIsersGln.....hslprthrAspAlaIserSergLusap 122
421  ACAGAGAAATGAACGCTGTGTAAATGACCAAGCAATCTTCTCAAAA 470
123  LeuLusSerFlaIlaAlaSerMetSergGlyCysLeuProFyMetLeuPfr 139
471  ACATAGAGAACTGCTGCGCTTCTCGATGCAATGGAACTCTACT 520
139  orFroLysCysProLanthrCysLeuAlaSerLysThrArgProLethus 156
521  GAAACAATGTCGCAAGCTGTATATGTCACAAATCAAGACCACTAGCT 570
156  lYtAlaCysAnkAlaArgAlaAlaProMetFrgGlyAlaSerAspAla 172
571  GCAATACCAATTAATTCACAAATGATATCTAGGATCATCAATCAACA 620
173  LeuAlaSerFrgProValLysGlyAlaSerGlyLusPfrLusPfr 189
621  CTCTGATCTCCAGCGCTCATATCAATGAAGAATGATGATGATGATGAT 670
189  glYtAlaAspProGlyPheLysLysThrArgLysPheProLusProVala 206
671  CGATGATGATGTCGAAACCTATAGAAACCACTATGATGATGATGATG 720
206  FrgLysLysThrArgLysValLysAlaSerAspLysValLysAsp 222
721  GAAGAATCTCCAGCACTATCAATGACCAAGCACTACTACTATTACAG 270
223  AspAspAspFyTrSerAspLysLeuMetAlaFrgLysGlyLysLysPhe 239
771  GATCTGATTAATCTCTATATCTGTGTGTGTGTGTGTGTGTGTGTGT 820
239  AspLysLysAlaPheThrFrgLysThrSerLysAlaAlaPheGlyLys 256
821  TGAATTTGATCTGACTTCAAGATGATGATGATGATGATGATGATGAT 870
256  lYtAspCysGlyLysMetThrCysGlyLysAlaAnProCysPheProIle 272
871  TGCAGATTTGCCCACTGACCTTCGCAATGATGACCTTCTCTCTATA 920
273  GluLysFrgLysLysAlaArgProAlaAlaLysThrAlaCysLeuProP 289
921  CTCTCTCGCGCGGATATCGAAGGCGGCTGCGCAATGCTCCCTCT 306
289  eYtArgSerSerAlaAlaCysGlyLysGlyAspGlyLysAlaLeuPhe 370
971  CTCAGATCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
306  lYsAlaSerSerThrAlaAnProFrgLysLysMetAspLysLysThr 322
1021  AGACACTC.....AGACACACACACACACACACACACACACACAC 1061
323  PheLysLeuThrValLysGlyLysSerProAlaLeuLysGly 339
1062  TCTCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1111
339  nLeuArgAspThrSerAlaLysLysLysLysLysLysLysLysLys 356
1112  TCTGAAATCTGATCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1161
356  eLysAsp.....SergLysAlaFyLysLysProPheValProProAla 371
1162  TTTATGACGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
372  ProAlaAlaCysAlaProLysLysLysLysLysLysLysLysLys 388
1209  ....CCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1252
388  cysPheLysAlaLysLysLysLysLysLysLysLysLysLysLys 405

```

```

1253  TTGTTTATCTCGGGAGACCCAGAGTTTCAGACAAATTTGACTATCAG 1302
445  lAlaLeuIsThrLeuLysPheArgGlyLysAlaAnArgLysLysAlaLeu 421
1303  CACTGACATTTATGGATAGACCAAGCAAGATTTGCTCGGAATG 1352
442  lYsAlaLeuAnAlaIstPsrAlaAlaAlaValaFrgLysLysLysLys 438
1353  AAGAAGATCCCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1402
443  gysValValGlyAlaLeuLysLysLysLysLysLysLysLysLys 455
1403  GAGATCTGTGGAGCTCTCTCATCTCATCTCATCTCATCTCATCTCAT 1452
455  rArgLysLysLysLysLysLysLysLysLysLysLysLysLysLys 471
1453  CAAGAATTTACGATGACTGGA.....ATGATCTCTCGCGAGATTC 1499
472  gYtYtAspSerThrAlaAnProThrValSerLeuValPheSerThrAl 488
1500  GATATCACCCGAGCGCTCAACCGACCATTCAGATTTTCCGACGG 1549
488  AlaPheAnPheGlyLysLysLysLysLysLysLysLysLysLysLys 505
1550  CGCATCTGATCTGCTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1599
505  sPAlaSerPheGlyLysLysLysLysLysLysLysLysLysLysLys 521
1600  ATGGAATTTACAGACATCTCAACGACAGCAAGCACTTTTGTGAG 1649
522  AlaPhePheProThrThrLeuLeuArgGlyLysLysLysLysLys 538
1650  GCATCTCTTTCGCTGTGGAATCATATACGAGGCTGTGACTCGAT 1699
538  lYtLeuArgGlyLysLysLysLysLysLysLysLysLysLysLysLys 555
1700  CTTCCGGGATGATTGGAAGAGCTGCCCAACTTAATCTGTGACAAA 1749
555  eLysMetLysLysLysLysLysLysLysLysLysLysLysLysLys 571
1750  TATCTACGAGAGAGCTGCGAAGAAGTTGTCAGATTCGAATAAGT 1799
572  ThrLeuAlaLeuAlaSerLysLeuLysLysLysLysLysLysLys 588
1800  GCTCTGATCTGCTCTCTCACTGAACCTCAACGAGCTGTGACAGCT 1849
588  uFrgLysFyLysLysLysLysLysLysLysLysLysLysLysLys 605
1850  CCACATTAATGATGCTGGAAGCAATTTGTACTTACAGAGATGGA 1899
605  hProAlaLysSerThrAlaAlaLysSerValAlaAspFyLys 621
1900  CATTGACCAATTTGCTCGAATGAGCTGCTGTGCTGTGCTGTGCTG 1949
622  lYsLeuAspLysLysLysLysLysLysLysLysLysLysLysLys 638
1950  TCGAGATATTAAGCGTCACTCTGCTGATCTGATCTGCTGCTGCTG 1999
638  lYsAlaLysLysLysLysLysLysLysLysLysLysLysLysLys 655
2000  CTGATGTGAGATCTGTGCTGTGGAATCGATGCTGACCACTTTCT 2049
655  yLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 671
2050  GCTCTCTACCAAGCAGCTGATCATCTCAGAGTGTGATAGTGTTC 2099
671  TFGPLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 688
2100  TATGAGCGGCTTCC.....ACCATGACATGATGAGGATTTGGAG 2143
688  sLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 705
2144  AATTCGCTGCTGCGAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2193

```


